SEQUENCE LISTING

<110> Lipton, Stuart A.
Okamoto, Shu-ichi

<120> Methods of Differentiating and
Protecting Cells By Modulating the P38/MEF2 Pathway

<130> P-LJ 4714

<140> US 09/876,187
<141> 2001-06-05

<150> US 60/209,539
<151> 2000-06-05

<160> 23

<170> FastSEQ for Windows Version 4.0

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ttggactaga agctgaaata acagaagctg tgtacgatgc attagggtat tgaagaaaat 360
taacttttga attaaatatt tggaatataa ggaaataagg aaagttgact gaaa atg 417
Met
1

ggg cgg aag aaa ata caa atc aca cgc ata atg gat gaa agg aac cga 465
Gly Arg Lys Lys Ile Gln Ile Thr Arg Ile Met Asp Glu Arg Asn Arg
5 10 15

cag gtc act ttt aca aag aga aag ttt gga tta atg aag aaa gcc tat 513
Gln Val Thr Phe Thr Lys Arg Lys Phe Gly Leu Met Lys Lys Ala Tyr
20 25 30

gaa ctt agt gtg ctc tgt gac tgt gaa ata gca ctc atc att ttc aac 561
Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe Asn
35 40 45

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agc tct aac aaa ctg ttt caa tat gct agc act gat atg gac aaa gtt   609
Ser Ser Asn Lys Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Lys Val
 50                  55                  60                  65

ctt ctc aag tat aca gaa tat aat gaa cct cat gaa agc aga acc aac   657
Leu Leu Lys Tyr Thr Glu Tyr Asn Glu Pro His Glu Ser Arg Thr Asn
                 70                  75                  80

tcg gat att gtt gag gct ctg aac aag aag gaa cac aga ggg tgc gac   705
Ser Asp Ile Val Glu Ala Leu Asn Lys Lys Glu His Arg Gly Cys Asp
             85                  90                  95

agc cca gac cct gat act tca tat gtg cta act cca cat aca gaa gaa   753
Ser Pro Asp Pro Asp Thr Ser Tyr Val Leu Thr Pro His Thr Glu Glu
        100                 105                 110

aaa tat aaa aaa att aat gag gaa ttt gat aat atg atg cgg aat cat   801
Lys Tyr Lys Lys Ile Asn Glu Glu Phe Asp Asn Met Met Arg Asn His
    115                 120                 125

aaa atc gca cct ggt ctg cca cct cag aac ttt tca atg tct gtc aca   849
Lys Ile Ala Pro Gly Leu Pro Pro Gln Asn Phe Ser Met Ser Val Thr
130                 135                 140                 145

gtt cca gtg acc agc ccc aat gct ttg tcc tac act aac cca ggg agt   897
Val Pro Val Thr Ser Pro Asn Ala Leu Ser Tyr Thr Asn Pro Gly Ser
                150                 155                 160

tca ctg gtg tcc cca tct ttg gca gcc agc tca acg tta aca gat tca   945
Ser Leu Val Ser Pro Ser Leu Ala Ala Ser Ser Thr Leu Thr Asp Ser
            165                 170                 175

agc atg ctc tct cca cct caa acc aca tta cat aga aat gtg tct cct   993
Ser Met Leu Ser Pro Pro Gln Thr Thr Leu His Arg Asn Val Ser Pro
        180                 185                 190

gga gct cct cag aga cca cca agt act ggc aat gca ggt ggg atg ttg   1041
Gly Ala Pro Gln Arg Pro Pro Ser Thr Gly Asn Ala Gly Gly Met Leu
    195                 200                 205

agc act aca gac ctc aca gtg cca aat gga gct gga agc agt cca gtg   1089
Ser Thr Thr Asp Leu Thr Val Pro Asn Gly Ala Gly Ser Ser Pro Val
210                 215                 220                 225

ggg aat gga ttt gta aac tca aga gct tct cca aat ttg att gga gct   1137
Gly Asn Gly Phe Val Asn Ser Arg Ala Ser Pro Asn Leu Ile Gly Ala
                230                 235                 240

act ggt gca aat agc tta ggc aaa gtc atg cct aca aag tct ccc cct   1185
Thr Gly Ala Asn Ser Leu Gly Lys Val Met Pro Thr Lys Ser Pro Pro
            245                 250                 255
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cca cca ggt ggt ggt aat ctt gga atg aac agt agg aaa cca gat ctt   1233
Pro Pro Gly Gly Gly Asn Leu Gly Met Asn Ser Arg Lys Pro Asp Leu
        260                 265                 270

cga gtt gtc atc ccc cct tca agc aag ggc atg atg cct cca cta tcg   1281
Arg Val Val Ile Pro Pro Ser Ser Lys Gly Met Met Pro Pro Leu Ser
    275                 280                 285

gag gaa gag gaa ttg gag ttg aac acc caa agg atc agt agt tct caa   1329
Glu Glu Glu Glu Leu Glu Leu Asn Thr Gln Arg Ile Ser Ser Ser Gln
290                 295                 300                 305

gcc act caa cct ctt gct acc cca gtc gtg tct gtg aca acc cca agc   1377
Ala Thr Gln Pro Leu Ala Thr Pro Val Val Ser Val Thr Thr Pro Ser
                310                 315                 320

ttg cct ccg caa gga ctt gtg tac tca gca atg ccg act gcc tac aac   1425
Leu Pro Pro Gln Gly Leu Val Tyr Ser Ala Met Pro Thr Ala Tyr Asn
            325                 330                 335

act gat tat tca ctg acc agc gct gac ctg tca gcc ctt caa ggc ttc   1473
Thr Asp Tyr Ser Leu Thr Ser Ala Asp Leu Ser Ala Leu Gln Gly Phe
        340                 345                 350

aac tcg cca gga atg ctg tcg ctg gga cag gtg tcg gcc tgg cag cag   1521
Asn Ser Pro Gly Met Leu Ser Leu Gly Gln Val Ser Ala Trp Gln Gln
    355                 360                 365

cac cac cta gga caa gca gcc ctc agc tct ctt gtt gct gga ggg cag   1569
His His Leu Gly Gln Ala Ala Leu Ser Ser Leu Val Ala Gly Gly Gln
370                 375                 380                 385

tta tct cag ggt tcc aat tta tcc att aat acc aac caa aac atc agc   1617
Leu Ser Gln Gly Ser Asn Leu Ser Ile Asn Thr Asn Gln Asn Ile Ser
                390                 395                 400

atc aag tcc gaa ccg att tca cct cct cgg gat cgt atg acc cca tcg   1665
Ile Lys Ser Glu Pro Ile Ser Pro Pro Arg Asp Arg Met Thr Pro Ser
            405                 410                 415

ggc ttc cag cag cag cag cag cag cag cag cag cag cag ccg ccg cca   1713
Gly Phe Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Pro Pro Pro
        420                 425                 430

cca ccg cag ccc cag cca caa ccc ccg cag ccc cag ccc cga cag gaa   1761
Pro Pro Gln Pro Gln Pro Gln Pro Pro Gln Pro Gln Pro Arg Gln Glu
    435                 440                 445

atg ggg cgc tcc cct gtg gac agt ctg agc agc tct agt agc tcc tat   1809
Met Gly Arg Ser Pro Val Asp Ser Leu Ser Ser Ser Ser Ser Ser Tyr
450                 455                 460                 465

gat ggc agt gat cgg gag gat cca cgg ggc gac ttc cat tct cca att   1857
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Asp Gly Ser Asp Arg Glu Asp Pro Arg Gly Asp Phe His Ser Pro Ile
                470                 475                 480

gtg ctt ggc cga ccc cca aac act gag gac aga gaa agc cct tct gta   1905
Val Leu Gly Arg Pro Pro Asn Thr Glu Asp Arg Glu Ser Pro Ser Val
            485                 490                 495

aag cga atg agg atg gac gcg tgg gtg acc taaggcttcc aagctgatgt     1955
Lys Arg Met Arg Met Asp Ala Trp Val Thr
        500                 505

ttgtactttt gtgttactgc agtgacctgc cctacatatc taaatcggta aataaggaca 2015
tgagttaaat atatttatat gtacatacat atatatatcc ctttacatat atatgtatgt 2075
gggtgtgagt gtgtgtgtat gtgtgggtgt gtgttacata cacagaatca ggcacttacc 2135
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<210> 2
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<212> PRT
<213> Homo sapiens

<400> 2

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Arg Gln Val Thr Phe Thr Lys Arg Lys Phe Gly Leu Met Lys Lys Ala
            20                  25                  30
Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe
        35                  40                  45
Asn Ser Ser Asn Lys Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Lys
    50                  55                  60
Val Leu Leu Lys Tyr Thr Glu Tyr Asn Glu Pro His Glu Ser Arg Thr
65                  70                  75                  80
Asn Ser Asp Ile Val Glu Ala Leu Asn Lys Lys Glu His Arg Gly Cys
                85                  90                  95
Asp Ser Pro Asp Pro Asp Thr Ser Tyr Val Leu Thr Pro His Thr Glu
            100                 105                 110
Glu Lys Tyr Lys Lys Ile Asn Glu Glu Phe Asp Asn Met Met Arg Asn
        115                 120                 125
His Lys Ile Ala Pro Gly Leu Pro Pro Gln Asn Phe Ser Met Ser Val
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    130                 135                 140
Thr Val Pro Val Thr Ser Pro Asn Ala Leu Ser Tyr Thr Asn Pro Gly
145                 150                 155                 160
Ser Ser Leu Val Ser Pro Ser Leu Ala Ala Ser Ser Thr Leu Thr Asp
                165                 170                 175
Ser Ser Met Leu Ser Pro Pro Gln Thr Thr Leu His Arg Asn Val Ser
            180                 185                 190
Pro Gly Ala Pro Gln Arg Pro Pro Ser Thr Gly Asn Ala Gly Gly Met
        195                 200                 205
Leu Ser Thr Thr Asp Leu Thr Val Pro Asn Gly Ala Gly Ser Ser Pro
    210                 215                 220
Val Gly Asn Gly Phe Val Asn Ser Arg Ala Ser Pro Asn Leu Ile Gly
225                 230                 235                 240
Ala Thr Gly Ala Asn Ser Leu Gly Lys Val Met Pro Thr Lys Ser Pro
                245                 250                 255
Pro Pro Pro Gly Gly Gly Asn Leu Gly Met Asn Ser Arg Lys Pro Asp
            260                 265                 270
Leu Arg Val Val Ile Pro Pro Ser Ser Lys Gly Met Met Pro Pro Leu
        275                 280                 285
Ser Glu Glu Glu Glu Leu Glu Leu Asn Thr Gln Arg Ile Ser Ser Ser
    290                 295                 300
Gln Ala Thr Gln Pro Leu Ala Thr Pro Val Val Ser Val Thr Thr Pro
305                 310                 315                 320
Ser Leu Pro Pro Gln Gly Leu Val Tyr Ser Ala Met Pro Thr Ala Tyr
                325                 330                 335
Asn Thr Asp Tyr Ser Leu Thr Ser Ala Asp Leu Ser Ala Leu Gln Gly
            340                 345                 350
Phe Asn Ser Pro Gly Met Leu Ser Leu Gly Gln Val Ser Ala Trp Gln
        355                 360                 365
Gln His His Leu Gly Gln Ala Ala Leu Ser Ser Leu Val Ala Gly Gly
    370                 375                 380
Gln Leu Ser Gln Gly Ser Asn Leu Ser Ile Asn Thr Asn Gln Asn Ile
385                 390                 395                 400
Ser Ile Lys Ser Glu Pro Ile Ser Pro Pro Arg Asp Arg Met Thr Pro
                405                 410                 415
Ser Gly Phe Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Pro Pro
            420                 425                 430
Pro Pro Pro Gln Pro Gln Pro Gln Pro Pro Gln Pro Gln Pro Arg Gln
        435                 440                 445
Glu Met Gly Arg Ser Pro Val Asp Ser Leu Ser Ser Ser Ser Ser Ser
    450                 455                 460
Tyr Asp Gly Ser Asp Arg Glu Asp Pro Arg Gly Asp Phe His Ser Pro
465                 470                 475                 480
Ile Val Leu Gly Arg Pro Pro Asn Thr Glu Asp Arg Glu Ser Pro Ser
                485                 490                 495
Val Lys Arg Met Arg Met Asp Ala Trp Val Thr
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<222> (443)...(1537)

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agcatgtgcg tcgctccctc cccgagctgg cccagcacaa ggcagacatg cagcgttggg 180
aggagcagag ccagggagcc atctacactg tggagtacgc ctgcagcgcc gtgaagaacc 240
tggtggacag cagcgtctac ttccgcagcg tggagggtct gctcaaacag gccatcagca 300
tccgggacca tatgaatgcc agtgcccagg gccacagccc ggaggaacca cccccgccct 360
cctcagcctg atcctggaag agactcgggg ccccccagcc tccgccaacc cagacaaaga 420
tcattccact cagcctggga cg atg ggg agg aaa aaa atc cag atc tcc cgc  472
                        Met Gly Arg Lys Lys Ile Gln Ile Ser Arg
                         1               5                  10

atc ctg gac caa agg aat cgg cag gtg acg ttc acc aag cgg aag ttc   520
Ile Leu Asp Gln Arg Asn Arg Gln Val Thr Phe Thr Lys Arg Lys Phe
                15                  20                  25

ggg ctg atg aag aag gcc tat gag ctg agc gtg ctc tgt gac tgt gag   568
Gly Leu Met Lys Lys Ala Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu
            30                  35                  40

ata gcc ctc atc atc ttc aac agc gcc aac cgc ctc ttc cag tat gcc   616
Ile Ala Leu Ile Ile Phe Asn Ser Ala Asn Arg Leu Phe Gln Tyr Ala
        45                  50                  55

agc acg gac atg gac cgt gtg ctg ctg aag tac aca gag tac agc gag   664
Ser Thr Asp Met Asp Arg Val Leu Leu Lys Tyr Thr Glu Tyr Ser Glu
    60                  65                  70

ccc cac gag agc cgc acc aac act gac atc ctc gag acg ctg aag cgg   712
Pro His Glu Ser Arg Thr Asn Thr Asp Ile Leu Glu Thr Leu Lys Arg
75                  80                  85                  90

agg ggc att ggc ctc gat ggg cca gag ctg gag ccg gat gaa ggg cct   760
Arg Gly Ile Gly Leu Asp Gly Pro Glu Leu Glu Pro Asp Glu Gly Pro
                95                  100                 105

gag gag cca gga gag aag ttt cgg agg ctg gca ggc gaa ggg ggt gat   808
Glu Glu Pro Gly Glu Lys Phe Arg Arg Leu Ala Gly Glu Gly Gly Asp
            110                 115                 120

ccg gcc ttg ccc cga ccc cgg ctg tat cct gca gct cct gct atg ccc   856
Pro Ala Leu Pro Arg Pro Arg Leu Tyr Pro Ala Ala Pro Ala Met Pro
        125                 130                 135

agc cca gat gtg gta tac ggg gcc tta ccg cca cca ggc tgt gac ccc   904
Ser Pro Asp Val Val Tyr Gly Ala Leu Pro Pro Pro Gly Cys Asp Pro
    140                 145                 150
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agt ggg ctt ggg gaa gca ctg ccc gcc cag agc cgc cca tct ccc ttc   952
Ser Gly Leu Gly Glu Ala Leu Pro Ala Gln Ser Arg Pro Ser Pro Phe
155                 160                 165                 170

cga cca gca gcc ccc aaa gcc ggg ccc cca ggc ctg gtg cac cct ctc   1000
Arg Pro Ala Ala Pro Lys Ala Gly Pro Pro Gly Leu Val His Pro Leu
                175                 180                 185

ttc tca cca agc cac ctc acc agc aag aca cca ccc cca ctg tac ctg   1048
Phe Ser Pro Ser His Leu Thr Ser Lys Thr Pro Pro Pro Leu Tyr Leu
            190                 195                 200

ccg acg gaa ggg cgg agg tca gac ctg cct ggt ggc ctg gct ggg ccc   1096
Pro Thr Glu Gly Arg Arg Ser Asp Leu Pro Gly Gly Leu Ala Gly Pro
        205                 210                 215

cga ggg gga cta aac acc tcc aga agc ctc tac agt ggc ctg cag aac   1144
Arg Gly Gly Leu Asn Thr Ser Arg Ser Leu Tyr Ser Gly Leu Gln Asn
    220                 225                 230

ccc tgc tcc act gca act ccc gga ccc cca ctg ggg agc ttc ccc ttc   1192
Pro Cys Ser Thr Ala Thr Pro Gly Pro Pro Leu Gly Ser Phe Pro Phe
235                 240                 245                 250

ctc ccc gga ggc ccc cca gtg ggg gcc gaa gcc tgg gcg agg agg gtc   1240
Leu Pro Gly Gly Pro Pro Val Gly Ala Glu Ala Trp Ala Arg Arg Val
                255                 260                 265

ccc caa ccc gcg gcg cct ccc cgc cga ccc ccc cag tca gca tca agt   1288
Pro Gln Pro Ala Ala Pro Pro Arg Arg Pro Pro Gln Ser Ala Ser Ser
            270                 275                 280

ctg agc gcc tct ctc cgg ccc ccg ggg gcc ccg gcg act ttc cta aga   1336
Leu Ser Ala Ser Leu Arg Pro Pro Gly Ala Pro Ala Thr Phe Leu Arg
        285                 290                 295

cct tcc cct atc cct tgc tcc tcg ccc ggt ccc tgg cag agc ctc tgc   1384
Pro Ser Pro Ile Pro Cys Ser Ser Pro Gly Pro Trp Gln Ser Leu Cys
    300                 305                 310

ggc ctg ggc ccg ccc tgc gcc ggc tgc cct tgg ccg acg gct ggc ccc   1432
Gly Leu Gly Pro Pro Cys Ala Gly Cys Pro Trp Pro Thr Ala Gly Pro
315                 320                 325                 330

ggt agg aga tca ccc ggt ggc acc agc cca gag cgc tcg cca ggt acg   1480
Gly Arg Arg Ser Pro Gly Gly Thr Ser Pro Glu Arg Ser Pro Gly Thr
                335                 340                 345

gcg agg gca cgt ggg gac ccc acc tcc ctc cag gcc tct tca gag aag   1528
Ala Arg Ala Arg Gly Asp Pro Thr Ser Leu Gln Ala Ser Ser Glu Lys
            350                 355                 360

acc caa cag tgacgccccc ctccgcggtg ggggcttgga ggtgggcggc           1577
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Thr Gln Gln
365

tggactcaat ccaccctggg gggctccttt ccttcttcct atttgtgtgt atatccacaa 1637
ataaaacgcg cgtggcgtcc gtggaccaaa aaaa 1671

<210> 4
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<212> PRT
<213> Homo sapiens

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Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe
35 40 45
Asn Ser Ala Asn Arg Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Arg
50 55 60
Val Leu Leu Lys Tyr Thr Glu Tyr Ser Glu Pro His Glu Ser Arg Thr
65 70 75 80
Asn Thr Asp Ile Leu Glu Thr Leu Lys Arg Arg Gly Ile Gly Leu Asp
85 90 95
Gly Pro Glu Leu Glu Pro Asp Glu Gly Pro Glu Glu Pro Gly Glu Lys
100 105 110
Phe Arg Arg Leu Ala Gly Glu Gly Gly Asp Pro Ala Leu Pro Arg Pro
115 120 125
Arg Leu Tyr Pro Ala Ala Pro Ala Met Pro Ser Pro Asp Val Val Tyr
130 135 140
Gly Ala Leu Pro Pro Pro Gly Cys Asp Pro Ser Gly Leu Gly Glu Ala
145 150 155 160
Leu Pro Ala Gln Ser Arg Pro Ser Pro Phe Arg Pro Ala Ala Pro Lys
165 170 175
Ala Gly Pro Pro Gly Leu Val His Pro Leu Phe Ser Pro Ser His Leu
180 185 190
Thr Ser Lys Thr Pro Pro Pro Leu Tyr Leu Pro Thr Glu Gly Arg Arg
195 200 205
Ser Asp Leu Pro Gly Gly Leu Ala Gly Pro Arg Gly Gly Leu Asn Thr
210 215 220
Ser Arg Ser Leu Tyr Ser Gly Leu Gln Asn Pro Cys Ser Thr Ala Thr
225 230 235 240
Pro Gly Pro Pro Leu Gly Ser Phe Pro Phe Leu Pro Gly Gly Pro Pro
245 250 255
Val Gly Ala Glu Ala Trp Ala Arg Arg Val Pro Gln Pro Ala Ala Pro
260 265 270
Pro Arg Arg Pro Pro Gln Ser Ala Ser Ser Leu Ser Ala Ser Leu Arg
275 280 285
Pro Pro Gly Ala Pro Ala Thr Phe Leu Arg Pro Ser Pro Ile Pro Cys
290 295 300
Ser Ser Pro Gly Pro Trp Gln Ser Leu Cys Gly Leu Gly Pro Pro Cys
305 310 315 320
Ala Gly Cys Pro Trp Pro Thr Ala Gly Pro Gly Arg Arg Ser Pro Gly

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                325                 330                 335
Gly Thr Ser Pro Glu Arg Ser Pro Gly Thr Ala Arg Ala Arg Gly Asp
            340                 345                 350
Pro Thr Ser Leu Gln Ala Ser Ser Glu Lys Thr Gln Gln
        355                 360                 365
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<210> 5
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<212> DNA
<213> Homo sapiens

<220>
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<222> (402)...(1820)

<400> 5

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ctgcatgttt gaatcaggtg gagaagcact tcaacgctgg acgaagtaaa gattattgtt 180
gttatttttt ttttctctct ctctctctct taagaaagga aaatatccca aggactaatc 240
tgatcgggtc ttccttcatc aggaacgaat gcaggaattt gggaactgag ctgtgcaagt 300
gctgaagaag gagatttgtt tggaggaaac aggaaagaga aagaaaagga aggaaaaaat 360
acataatttc agggacgaga gagagaagaa aaacggggac t atg ggg aga aaa aag 416
                                            Met Gly Arg Lys Lys
                                             1               5

att cag att acg agg att atg gat gaa cgt aac aga cag gtg aca ttt   464
Ile Gln Ile Thr Arg Ile Met Asp Glu Arg Asn Arg Gln Val Thr Phe
                10                  15                  20

aca aag agg aaa ttt ggg ttg atg aag aag gct tat gag ctg agc gtg   512
Thr Lys Arg Lys Phe Gly Leu Met Lys Lys Ala Tyr Glu Leu Ser Val
            25                  30                  35

ctg tgt gac tgt gag att gcg ctg atc atc ttc aac agc acc aac aag   560
Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe Asn Ser Thr Asn Lys
        40                  45                  50

ctg ttc cag tat gcc agc acc gac atg gac aaa gtg ctt ctc aag tac   608
Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Lys Val Leu Leu Lys Tyr
    55                  60                  65

acg gag tac aac gag ccg cat gag agc cgg aca aac tca gac atc gtg   656
Thr Glu Tyr Asn Glu Pro His Glu Ser Arg Thr Asn Ser Asp Ile Val
70                  75                  80                  85

gag acg ttg aga aag aag ggc ctt aat ggc tgt gac agc cca gac ccc   704
Glu Thr Leu Arg Lys Lys Gly Leu Asn Gly Cys Asp Ser Pro Asp Pro
                90                  95                  100

gat gcg gac gat tcc gta ggt cac agc cct gag tct gag gac aag tac   752
Asp Ala Asp Asp Ser Val Gly His Ser Pro Glu Ser Glu Asp Lys Tyr
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            105                 110                 115

agg aaa att aac gaa gat att gat cta atg atc agc agg caa aga ttg   800
Arg Lys Ile Asn Glu Asp Ile Asp Leu Met Ile Ser Arg Gln Arg Leu
        120                 125                 130

tgt gct gtt cca cct ccc aac ttc gag atg cca gtc tcc atc cca gtg   848
Cys Ala Val Pro Pro Pro Asn Phe Glu Met Pro Val Ser Ile Pro Val
    135                 140                 145

tcc agc cac aac agt ttg gtg tac agc aac cct gtc agc tca ctg gga   896
Ser Ser His Asn Ser Leu Val Tyr Ser Asn Pro Val Ser Ser Leu Gly
150                 155                 160                 165

aac ccc aac cta ttg cca ctg gct cac cct tct ctg cag agg aat agt   944
Asn Pro Asn Leu Leu Pro Leu Ala His Pro Ser Leu Gln Arg Asn Ser
                170                 175                 180

atg tct cct ggt gta aca cat cga cct cca agt gca ggt aac aca ggt   992
Met Ser Pro Gly Val Thr His Arg Pro Pro Ser Ala Gly Asn Thr Gly
            185                 190                 195

ggt ctg atg ggt gga gac ctc acg tct ggt gca ggc acc agt gca ggg   1040
Gly Leu Met Gly Gly Asp Leu Thr Ser Gly Ala Gly Thr Ser Ala Gly
        200                 205                 210

aac ggg tat ggc aat ccc cga aac tca cca ggt ctg ctg gtc tca cct   1088
Asn Gly Tyr Gly Asn Pro Arg Asn Ser Pro Gly Leu Leu Val Ser Pro
    215                 220                 225

ggt aac ttg aac aag aat atg caa gca aaa tct cct ccc cca atg aat   1136
Gly Asn Leu Asn Lys Asn Met Gln Ala Lys Ser Pro Pro Pro Met Asn
230                 235                 240                 245

tta gga atg aat aac cgt aaa cca gat ctc cga gtt ctt att cca cca   1184
Leu Gly Met Asn Asn Arg Lys Pro Asp Leu Arg Val Leu Ile Pro Pro
                250                 255                 260

ggc agc aag aat acg atg cca tca gtg tct gag gat gtc gac ctg ctt   1232
Gly Ser Lys Asn Thr Met Pro Ser Val Ser Glu Asp Val Asp Leu Leu
            265                 270                 275

ttg aat caa agg ata aat aac tcc cag tcg gct cag tca ttg gct acc   1280
Leu Asn Gln Arg Ile Asn Asn Ser Gln Ser Ala Gln Ser Leu Ala Thr
        280                 285                 290

cca gtg gtt tcc gta gca act cct act tta cca gga caa gga atg gga   1328
Pro Val Val Ser Val Ala Thr Pro Thr Leu Pro Gly Gln Gly Met Gly
    295                 300                 305

gga tat cca tca gcc att tca aca aca tat ggt acc gag tac tct ctg   1376
Gly Tyr Pro Ser Ala Ile Ser Thr Thr Tyr Gly Thr Glu Tyr Ser Leu
310                 315                 320                 325
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agt agt gca gac ctg tca tct ctg tct ggg ttt aac acc gcc agc gct   1424
Ser Ser Ala Asp Leu Ser Ser Leu Ser Gly Phe Asn Thr Ala Ser Ala
                330                 335                 340

ctt cac ctt ggt tca gta act ggc tgg caa cag caa cac cta cat aac   1472
Leu His Leu Gly Ser Val Thr Gly Trp Gln Gln Gln His Leu His Asn
            345                 350                 355

atg cca cca tct gcc ctc agt cag ttg gga gct tgc act agc act cat   1520
Met Pro Pro Ser Ala Leu Ser Gln Leu Gly Ala Cys Thr Ser Thr His
        360                 365                 370

tta tct cag agt tca aat ctc tcc ctg cct tct act caa agc ctc aac   1568
Leu Ser Gln Ser Ser Asn Leu Ser Leu Pro Ser Thr Gln Ser Leu Asn
    375                 380                 385

atc aag tca gaa cct gtt tct cct cct aga gac cgt acc acc acc cct   1616
Ile Lys Ser Glu Pro Val Ser Pro Pro Arg Asp Arg Thr Thr Thr Pro
390                 395                 400                 405

tcg aga tac cca caa cac acg cgc cac gag gcg ggg aga tct cct gtt   1664
Ser Arg Tyr Pro Gln His Thr Arg His Glu Ala Gly Arg Ser Pro Val
                410                 415                 420

gac agc ttg agc agc tgt agc agt tcg tac gac ggg agc gac cga gag   1712
Asp Ser Leu Ser Ser Cys Ser Ser Ser Tyr Asp Gly Ser Asp Arg Glu
            425                 430                 435

gat cac cgg aac gaa ttc cac tcc ccc att gga ctc acc aga cct tcg   1760
Asp His Arg Asn Glu Phe His Ser Pro Ile Gly Leu Thr Arg Pro Ser
        440                 445                 450

ccg gac gaa agg gaa agt ccc tca gtc aag cgc atg cga ctt tct gaa   1808
Pro Asp Glu Arg Glu Ser Pro Ser Val Lys Arg Met Arg Leu Ser Glu
    455                 460                 465

gga tgg gca aca tgatcagatt attacttact agttttttt tttttcttgc       1860
Gly Trp Ala Thr
470

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<213> Homo sapiens

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Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe
        35                  40                  45
Asn Ser Thr Asn Lys Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Lys
    50                  55                  60
Val Leu Leu Lys Tyr Thr Glu Tyr Asn Glu Pro His Glu Ser Arg Thr
65                  70                  75                  80
Asn Ser Asp Ile Val Glu Thr Leu Arg Lys Lys Gly Leu Asn Gly Cys
                85                  90                  95
Asp Ser Pro Asp Pro Asp Ala Asp Asp Ser Val Gly His Ser Pro Glu
            100                 105                 110
Ser Glu Asp Lys Tyr Arg Lys Ile Asn Glu Asp Ile Asp Leu Met Ile
        115                 120                 125
Ser Arg Gln Arg Leu Cys Ala Val Pro Pro Pro Asn Phe Glu Met Pro
    130                 135                 140
Val Ser Ile Pro Val Ser Ser His Asn Ser Leu Val Tyr Ser Asn Pro
145                 150                 155                 160
Val Ser Ser Leu Gly Asn Pro Asn Leu Leu Pro Leu Ala His Pro Ser
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```
                165                 170                 175
Leu Gln Arg Asn Ser Met Ser Pro Gly Val Thr His Arg Pro Pro Ser
            180                 185                 190
Ala Gly Asn Thr Gly Gly Leu Met Gly Gly Asp Leu Thr Ser Gly Ala
        195                 200                 205
Gly Thr Ser Ala Gly Asn Gly Tyr Gly Asn Pro Arg Asn Ser Pro Gly
    210                 215                 220
Leu Leu Val Ser Pro Gly Asn Leu Asn Lys Asn Met Gln Ala Lys Ser
225                 230                 235                 240
Pro Pro Pro Met Asn Leu Gly Met Asn Asn Arg Lys Pro Asp Leu Arg
                245                 250                 255
Val Leu Ile Pro Pro Gly Ser Lys Asn Thr Met Pro Ser Val Ser Glu
            260                 265                 270
Asp Val Asp Leu Leu Leu Asn Gln Arg Ile Asn Asn Ser Gln Ser Ala
        275                 280                 285
Gln Ser Leu Ala Thr Pro Val Val Ser Val Ala Thr Pro Thr Leu Pro
    290                 295                 300
Gly Gln Gly Met Gly Gly Tyr Pro Ser Ala Ile Ser Thr Thr Tyr Gly
305                 310                 315                 320
Thr Glu Tyr Ser Leu Ser Ser Ala Asp Leu Ser Ser Leu Ser Gly Phe
                325                 330                 335
Asn Thr Ala Ser Ala Leu His Leu Gly Ser Val Thr Gly Trp Gln Gln
            340                 345                 350
Gln His Leu His Asn Met Pro Pro Ser Ala Leu Ser Gln Leu Gly Ala
        355                 360                 365
Cys Thr Ser Thr His Leu Ser Gln Ser Ser Asn Leu Ser Leu Pro Ser
    370                 375                 380
Thr Gln Ser Leu Asn Ile Lys Ser Glu Pro Val Ser Pro Pro Arg Asp
385                 390                 395                 400
Arg Thr Thr Thr Pro Ser Arg Tyr Pro Gln His Thr Arg His Glu Ala
                405                 410                 415
Gly Arg Ser Pro Val Asp Ser Leu Ser Ser Cys Ser Ser Ser Tyr Asp
            420                 425                 430
Gly Ser Asp Arg Glu Asp His Arg Asn Glu Phe His Ser Pro Ile Gly
        435                 440                 445
Leu Thr Arg Pro Ser Pro Asp Glu Arg Glu Ser Pro Ser Val Lys Arg
    450                 455                 460
Met Arg Leu Ser Glu Gly Trp Ala Thr
465                 470
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<210> 7
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<213> Homo sapiens

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tgatcgggtc ttccttcatc aggaacgaat gcaggaattt gggaactgag ctgtgcaagt 300
gctgaagaag gagatttgtt tggaggaaac aggaaagaga aagaaaagga aggaaaaaat 360
acataatttc agggacgaga gagagaagaa aaacggggac t atg ggg aga aaa aag 416
                                              Met Gly Arg Lys Lys
                                               1               5

att cag att acg agg att atg gat gaa cgt aac aga cag gtg aca ttt   464
Ile Gln Ile Thr Arg Ile Met Asp Glu Arg Asn Arg Gln Val Thr Phe
                10                  15                  20

aca aag agg aaa ttt ggg ttg atg aag aag gct tat gag ctg agc gtg   512
Thr Lys Arg Lys Phe Gly Leu Met Lys Lys Ala Tyr Glu Leu Ser Val
            25                  30                  35

ctg tgt gac tgt gag att gcg ctg atc atc ttc aac agc acc aac aag   560
Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe Asn Ser Thr Asn Lys
        40                  45                  50

ctg ttc cag tat gcc agc acc gac atg gac aaa gtg ctt ctc aag tac   608
Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Lys Val Leu Leu Lys Tyr
    55                  60                  65

acg gag tac aac gag ccg cat gag agc cgg aca aac tca gac atc gtg   656
Thr Glu Tyr Asn Glu Pro His Glu Ser Arg Thr Asn Ser Asp Ile Val
70                  75                  80                  85

gag acg ttg aga aag aag ggc ctt aat ggc tgt gac agc cca gac ccc   704
Glu Thr Leu Arg Lys Lys Gly Leu Asn Gly Cys Asp Ser Pro Asp Pro
                90                  95                  100

gat gcg gac gat tcc gta ggt cac agc cct gag tct gag gac aag tac   752
Asp Ala Asp Asp Ser Val Gly His Ser Pro Glu Ser Glu Asp Lys Tyr
            105                 110                 115

agg aaa att aac gaa gat att gat cta atg atc agc agg caa aga ttg   800
Arg Lys Ile Asn Glu Asp Ile Asp Leu Met Ile Ser Arg Gln Arg Leu
        120                 125                 130

tgt gct gtt cca cct ccc aac ttc gag atg cca gtc tcc atc cca gtg   848
Cys Ala Val Pro Pro Pro Asn Phe Glu Met Pro Val Ser Ile Pro Val
    135                 140                 145

tcc agc cac aac agt ttg gtg tac agc aac cct gtc agc tca ctg gga   896
Ser Ser His Asn Ser Leu Val Tyr Ser Asn Pro Val Ser Ser Leu Gly
150                 155                 160                 165

aac ccc aac cta ttg cca ctg gct cac cct tct ctg cag agg aat agt   944
Asn Pro Asn Leu Leu Pro Leu Ala His Pro Ser Leu Gln Arg Asn Ser
                170                 175                 180

atg tct cct ggt gta aca cat cga cct cca agt gca ggt aac aca ggt   992
```

```
Met Ser Pro Gly Val Thr His Arg Pro Pro Ser Ala Gly Asn Thr Gly
            185                 190                 195

ggt ctg atg ggt gga gac ctc acg tct ggt gca ggc acc agt gca ggg   1040
Gly Leu Met Gly Gly Asp Leu Thr Ser Gly Ala Gly Thr Ser Ala Gly
        200                 205                 210

aac ggg tat ggc aat ccc cga aac tca cca ggt ctg ctg gtc tca cct   1088
Asn Gly Tyr Gly Asn Pro Arg Asn Ser Pro Gly Leu Leu Val Ser Pro
    215                 220                 225

ggt aac ttg aac aag aat atg caa gca aaa tct cct ccc cca atg aat   1136
Gly Asn Leu Asn Lys Asn Met Gln Ala Lys Ser Pro Pro Pro Met Asn
230                 235                 240                 245

tta gga atg aat aac cgt aaa cca gat ctc cga gtt ctt att cca cca   1184
Leu Gly Met Asn Asn Arg Lys Pro Asp Leu Arg Val Leu Ile Pro Pro
                250                 255                 260

ggc agc aag aat acg atg cca tca gtg tct gag gat gtc gac ctg ctt   1232
Gly Ser Lys Asn Thr Met Pro Ser Val Ser Glu Asp Val Asp Leu Leu
            265                 270                 275

ttg aat caa agg ata aat aac tcc cag tcg gct cag tca ttg gct acc   1280
Leu Asn Gln Arg Ile Asn Asn Ser Gln Ser Ala Gln Ser Leu Ala Thr
        280                 285                 290

cca gtg gtt tcc gta gca act cct act tta cca gga caa gga atg gga   1328
Pro Val Val Ser Val Ala Thr Pro Thr Leu Pro Gly Gln Gly Met Gly
    295                 300                 305

gga tat cca tca gcc att tca aca aca tat ggt acc gag tac tct ctg   1376
Gly Tyr Pro Ser Ala Ile Ser Thr Thr Tyr Gly Thr Glu Tyr Ser Leu
310                 315                 320                 325

agt agt gca gac ctg tca tct ctg tct ggg ttt aac acc gcc agc gct   1424
Ser Ser Ala Asp Leu Ser Ser Leu Ser Gly Phe Asn Thr Ala Ser Ala
                330                 335                 340

ctt cac ctt ggt tca gta act ggc tgg caa cag caa cac cta cat aac   1472
Leu His Leu Gly Ser Val Thr Gly Trp Gln Gln Gln His Leu His Asn
            345                 350                 355

atg cca cca tct gcc ctc agt cag ttg gga gct tgc act agc act cat   1520
Met Pro Pro Ser Ala Leu Ser Gln Leu Gly Ala Cys Thr Ser Thr His
        360                 365                 370

tta tct cag agt tca aat ctc tcc ctg cct tct act caa agc ctc aac   1568
Leu Ser Gln Ser Ser Asn Leu Ser Leu Pro Ser Thr Gln Ser Leu Asn
    375                 380                 385

atc aag tca gaa cct gtt tct cct cct aga gac cgt acc acc acc cct   1616
Ile Lys Ser Glu Pro Val Ser Pro Pro Arg Asp Arg Thr Thr Thr Pro
```

```
390                 395                 400                 405

tcg aga tac cca caa cac acg cgc cac gag gcg ggg aga tct cct gtt   1664
Ser Arg Tyr Pro Gln His Thr Arg His Glu Ala Gly Arg Ser Pro Val
                410                 415                 420

gac agc ttg agc agc tgt agc agt tcg tac gac ggg agc gac cga gag   1712
Asp Ser Leu Ser Ser Cys Ser Ser Ser Tyr Asp Gly Ser Asp Arg Glu
            425                 430                 435

gat cac cgg aac gaa ttc cac tcc ccc att gga ctc acc aga cct tcg   1760
Asp His Arg Asn Glu Phe His Ser Pro Ile Gly Leu Thr Arg Pro Ser
        440                 445                 450

ccg gac gaa agg gaa agt ccc tca gtc aag cgc atg cga ctt tct gaa   1808
Pro Asp Glu Arg Glu Ser Pro Ser Val Lys Arg Met Arg Leu Ser Glu
    455                 460                 465

gga tgg gca aca tgatcagatt attacttact agttttttt tttttcttgc       1860
Gly Trp Ala Thr
470

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<210> 8
<211> 473
<212> PRT
<213> Homo sapiens

<400> 8

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			20					25				30			
Tyr	Glu	Leu	Ser	Val	Leu	Cys	Asp	Cys	Glu	Ile	Ala	Leu	Ile	Ile	Phe
		35					40					45			
Asn	Ser	Thr	Asn	Lys	Leu	Phe	Gln	Tyr	Ala	Ser	Thr	Asp	Met	Asp	Lys
	50					55					60				
Val	Leu	Leu	Lys	Tyr	Thr	Glu	Tyr	Asn	Glu	Pro	His	Glu	Ser	Arg	Thr
65					70					75					80
Asn	Ser	Asp	Ile	Val	Glu	Thr	Leu	Arg	Lys	Lys	Gly	Leu	Asn	Gly	Cys
				85					90					95	
Asp	Ser	Pro	Asp	Pro	Asp	Ala	Asp	Asp	Ser	Val	Gly	His	Ser	Pro	Glu
			100					105					110		
Ser	Glu	Asp	Lys	Tyr	Arg	Lys	Ile	Asn	Glu	Asp	Ile	Asp	Leu	Met	Ile
		115					120					125			
Ser	Arg	Gln	Arg	Leu	Cys	Ala	Val	Pro	Pro	Pro	Asn	Phe	Glu	Met	Pro
	130					135					140				
Val	Ser	Ile	Pro	Val	Ser	Ser	His	Asn	Ser	Leu	Val	Tyr	Ser	Asn	Pro
145					150					155					160
Val	Ser	Ser	Leu	Gly	Asn	Pro	Asn	Leu	Leu	Pro	Leu	Ala	His	Pro	Ser
				165					170					175	
Leu	Gln	Arg	Asn	Ser	Met	Ser	Pro	Gly	Val	Thr	His	Arg	Pro	Pro	Ser
			180					185					190		
Ala	Gly	Asn	Thr	Gly	Gly	Leu	Met	Gly	Gly	Asp	Leu	Thr	Ser	Gly	Ala
		195					200					205			
Gly	Thr	Ser	Ala	Gly	Asn	Gly	Tyr	Gly	Asn	Pro	Arg	Asn	Ser	Pro	Gly
	210					215					220				
Leu	Leu	Val	Ser	Pro	Gly	Asn	Leu	Asn	Lys	Asn	Met	Gln	Ala	Lys	Ser
225					230					235					240
Pro	Pro	Pro	Met	Asn	Leu	Gly	Met	Asn	Asn	Arg	Lys	Pro	Asp	Leu	Arg
				245					250					255	
Val	Leu	Ile	Pro	Pro	Gly	Ser	Lys	Asn	Thr	Met	Pro	Ser	Val	Ser	Glu
			260					265					270		
Asp	Val	Asp	Leu	Leu	Leu	Asn	Gln	Arg	Ile	Asn	Asn	Ser	Gln	Ser	Ala
		275					280					285			
Gln	Ser	Leu	Ala	Thr	Pro	Val	Val	Ser	Val	Ala	Thr	Pro	Thr	Leu	Pro
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Gly	Gln	Gly	Met	Gly	Gly	Tyr	Pro	Ser	Ala	Ile	Ser	Thr	Thr	Tyr	Gly
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Thr Glu Tyr Ser Leu Ser Ser Ala Asp Leu Ser Ser Leu Ser Gly Phe
                325                 330                 335
Asn Thr Ala Ser Ala Leu His Leu Gly Ser Val Thr Gly Trp Gln Gln
            340                 345                 350
Gln His Leu His Asn Met Pro Pro Ser Ala Leu Ser Gln Leu Gly Ala
        355                 360                 365
Cys Thr Ser Thr His Leu Ser Gln Ser Ser Asn Leu Ser Leu Pro Ser
    370                 375                 380
Thr Gln Ser Leu Asn Ile Lys Ser Glu Pro Val Ser Pro Pro Arg Asp
385                 390                 395                 400
Arg Thr Thr Thr Pro Ser Arg Tyr Pro Gln His Thr Arg His Glu Ala
                405                 410                 415
Gly Arg Ser Pro Val Asp Ser Leu Ser Ser Cys Ser Ser Ser Tyr Asp
            420                 425                 430
Gly Ser Asp Arg Glu Asp His Arg Asn Glu Phe His Ser Pro Ile Gly
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Leu Thr Arg Pro Ser Pro Asp Glu Arg Glu Ser Pro Ser Val Lys Arg
    450                 455                 460
Met Arg Leu Ser Glu Gly Trp Ala Thr
465                 470
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<213> Homo sapiens

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<210> 10
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Thr Glu Asp His Leu Asp Leu
 1   5

<210> 11
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<212> PRT
<213> Homo sapiens

<400> 11
Ser Glu Asp Val Asp Leu Leu Leu
 1   5

<210> 12

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<220>
<223> synthetic

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<210> 13
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<212> PRT
<213> Homo sapiens

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Xaa Arg Lys Pro Asp Leu Arg Val Val
20 25

<210> 14
<211> 39
<212> PRT
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<400> 14
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Val Tyr Ser Ala Met Pro Thr Ala Tyr Asn Thr Asp Tyr Ser Leu Thr
20 25 30
Ser Ala Asp Leu Ser Ala Leu
35

<210> 15
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<400> 15
Ile Ser Ile Lys Ser Glu Pro Ile Ser Pro Pro Arg Asp Arg
1 5 10

<210> 16
<211> 22

<212> PRT
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<400> 16
Gly Arg Ser Pro Val Asp Ser Leu Ser Ser Ser Ser Ser Ser Tyr Asp
 1   5   10   15
Gly Ser Asp Arg Glu Asp
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<210> 17
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<220>
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Arg Asp Leu Arg Val Leu
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<211> 41
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<213> Homo sapiens

<400> 18
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Gly Gly Tyr Pro Ser Ala Ile Ser Thr Thr Tyr Gly Thr Glu Tyr Ser
            20   25   30
Leu Ser Ser Ala Asp Leu Ser Ser Leu
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<400> 19
Leu Ser Ile Lys Ser Glu Pro Val Ser Pro Pro Arg Asp Arg
 1   5   10

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<212> PRT
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<400> 20
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1 5 10 15
Asp Ser Asp Arg Glu Asp
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Xaa Xaa Arg Lys Pro Asp Leu Arg Val Ile
20 25

<210> 22
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1 5 10 15
Pro Phe Ser Ser Met Pro Thr Ala Tyr Asn Thr Asp Tyr Gln Leu Pro
20 25 30
Ser Ala Glu Leu Ser Ser Leu
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Ile Ser Ile Lys Ser Glu Pro Val Ser Pro Ser Arg Glu Arg
1 5 10